



Query= SEQ ID NO:1
(3963 letters)

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Sequences producing significant alignments:

Score E
(bits) Value

AC024258.9.1.160658
AL512429.14.1.11170
AC016395.5.1.166869

1794 0.0
1159 0.0
442 e-121

>AC024258.9.1.160658
Length = 160658

RECEIVED

SEP 04 2003

Score = 1794 bits (904), Expect = 0.0
Identities = 904/904 (100%)
Strand = Plus / Plus

TECH CENTER 1600/2900

Query: 1 atgcaagacgacgacatagaagcttctacttccatatctcagcttctaagagagagctat 60
|||||
Sbjct: 110106 atgcaagacgacgacatagaagcttctacttccatatctcagcttctaagagagagctat 110165

Query: 61 ttagctgaaaccagacatcggggaaacaatgagaggagtcgagcggagccctcctccaac 120
|||||
Sbjct: 110166 ttagctgaaaccagacatcggggaaacaatgagaggagtcgagcggagccctcctccaac 110225

Query: 121 ccttgccatttcggcagtccttctggggccgctgaaggaggcggaggccaagatgacctt 180
|||||
Sbjct: 110226 ccttgccatttcggcagtccttctggggccgctgaaggaggcggaggccaagatgacctt 110285

Query: 181 ccagatctttcagcctttctgagccaagaagaattagacgaaagtgtcaatttggcaaga 240
|||||
Sbjct: 110286 ccagatctttcagcctttctgagccaagaagaattagacgaaagtgtcaatttggcaaga 110345

Query: 241 ctggccatcaattacgaccctttggagaaggcagatgaaactcaagctagaaaaacgactt 300
|||||
Sbjct: 110346 ctggccatcaattacgaccctttggagaaggcagatgaaactcaagctagaaaaacgactt 110405

Query: 301 tctcctgatcagatgaaacactcacctaatttaagttttgagcctaacttctgccaggat 360
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Sbjct: 110406 tctcctgatcagatgaaacactcacctaatttaagttttgagcctaacttctgccaggat 110465

Query: 361 aaccctcgaagtcccaccagctctaaagaaagccccaggaggcaaaaaggccacagtat 420
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Sbjct: 110466 aaccctcgaagtcccaccagctctaaagaaagccccaggaggcaaaaaggccacagtat 110525

Query: 421 tgttctgaaaccagtcacaaaaaagtatttttaataaggctgccgacttcattgaagag 480
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Sbjct: 110526 tgttctgaaaccagtcacaaaaaagtatttttaataaggctgccgacttcattgaagag 110585

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|||||
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Query: 601 gatctgtcagaaagacgagaaagatcttctgttcccatccctatccctgcggataaccagg 660
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Sbjct: 110706 gatctgtcagaaagacgagaaagatcttctgttcccatccctatccctgcggataaccagg 110765

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Sbjct: 110886 tatgaagaacctctggggcaacctccccgggttcaactcaaaagttacggagcagagaagtt 110945

Query: 841 ccagaaggaactcgagtacagttggattgcatagtggtaggaattccaccacctcaagta 900
|||||
Sbjct: 110946 ccagaaggaactcgagtacagttggattgcatagtggtaggaattccaccacctcaagta 111005

Query: 901 aggt 904
||||
Sbjct: 111006 aggt 111009

Score = 728 bits (367), Expect = 0.0
Identities = 372/375 (99%)
Strand = Plus / Plus

Query: 1599 aggaaatgaggacctcagcaacaacgggtctcttcaactcagccaactcyaccaccaacct 1658
|||||
Sbjct: 154959 aggaaatgaggacctcagcaacaacgggtctcttcaactcagccaactctaccaccaacct 155018

Query: 1659 ggcagctattgagccacagccctccccacccactcagagcctccatctgtggaacaacc 1718
|||||
Sbjct: 155019 ggcagctattgagccacagccctccccacccactcagagcctccatctgtggaacaacc 155078

Query: 1719 ccccaaaccctcgaggggttctggtgaaccacaatgagccccggtccagctccag 1778
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Sbjct: 155079 ccccaaaccctcgaggggttctggtgaaccacaatgagccccggtccagctccag 155138

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|||||
Sbjct: 155139 gattgggcttcgtgtgcacttcaacctgcctgaagatgacaaaggaagtgaagcatcctc 155198

Query: 1839 cgaggctggtgtggtgaccaccagacagaccaggccccgattctttscaggagaggttcaa 1898
|||||
Sbjct: 155199 cgaggctggtgtggtgaccaccagacagaccaggccccgattctttccaggagaggttcaa 155258

Query: 1899 cggacaggcaacaaaaaccccagagccttctttccccgtgaaagagccccctccagttct 1958
|||||
Sbjct: 155259 cggacaggcaacaaaaaccccagagccttctttccccgtgaaagagccccctccagttct 155318

Query: 1959 ggccaaaccctaaact 1973
|||||
Sbjct: 155319 ggccaaaccctaaact 155333

Score = 355 bits (179), Expect = 1e-94
Identities = 179/179 (100%)
Strand = Plus / Plus

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|||||
Sbjct: 131605 aggtggtactgtgaaggcaaggagcttgaaaattccccagatattcacatcgtccaggca 131664

Query: 961 ggaaatctgcactcactgaccattgcggaagcctttgaagaggacacaggacgctattcc 1020
|||||
Sbjct: 131665 ggaaatctgcactcactgaccattgcggaagcctttgaagaggacacaggacgctattcc 131724

Query: 1021 tgctttgcttctaacaatctatgggacagattcgacttctgctgagatttatatagaagg 1079
|||||
Sbjct: 131725 tgctttgcttctaacaatctatgggacagattcgacttctgctgagatttatatagaagg 131783

Score = 286 bits (144), Expect = 9e-74
Identities = 144/144 (100%)
Strand = Plus / Plus

Query: 1316 agatgctacaaaatttgtcagcttctgagggtcagctggttgtctttgaatgcagagtaa 1375
|||||
Sbjct: 147151 agatgctacaaaatttgtcagcttctgagggtcagctggttgtctttgaatgcagagtaa 147210

Query: 1376 aaggagctccatctcctaaggttgagtggatatagagaagggactttaatagaagattctc 1435
|||||
Sbjct: 147211 aaggagctccatctcctaaggttgagtggatatagagaagggactttaatagaagattctc 147270

Query: 1436 cagattttaggattttacagaaaa 1459
|||||
Sbjct: 147271 cagattttaggattttacagaaaa 147294

Score = 238 bits (120), Expect = 2e-59
Identities = 120/120 (100%)
Strand = Plus / Plus

Query: 1482 agaggagatttgacaccttggtcattgctgaggtgtttgcagaagattctgggtgcttcac 1541
|||||
Sbjct: 154367 agaggagatttgacaccttggtcattgctgaggtgtttgcagaagattctgggtgcttcac 154426

Query: 1542 atgtactgcaagcaacaaatacggcacagtgtcaagcattgcacagctgcacgtgagagg 1601
|||||
Sbjct: 154427 atgtactgcaagcaacaaatacggcacagtgtcaagcattgcacagctgcacgtgagagg 154486

Score = 230 bits (116), Expect = 5e-57
Identities = 116/116 (100%)
Strand = Plus / Plus

Query: 1130 gaatccagaagccaaatgaggtgtcatctcctcccactacctctgcagtcattcctccag 1189
|||||
Sbjct: 137019 gaatccagaagccaaatgaggtgtcatctcctcccactacctctgcagtcattcctccag 137078

Query: 1190 cagtaccccaagcccagcatttggtggcccaacctcgtgtggcaaccatccagcag 1245
|||||
Sbjct: 137079 cagtaccccaagcccagcatttggtggcccaacctcgtgtggcaaccatccagcag 137134

Score = 149 bits (75), Expect = 1e-32
Identities = 75/75 (100%)
Strand = Plus / Plus

Query: 1243 cagtgtcagagccccaccaattacttgagggttgatggaaaacctatcattgcagct 1302
|||||
Sbjct: 138704 cagtgtcagagccccaccaattacttgagggttgatggaaaacctatcattgcagct 138763

Query: 1303 cctgtgtttacaaag 1317
|||||
Sbjct: 138764 cctgtgtttacaaag 138778

Score = 107 bits (54), Expect = 5e-20
Identities = 54/54 (100%)
Strand = Plus / Plus

Query: 1077 agggggtttcttcttctgactcagaaggcgaccctaacaaggaagagatgaatcg 1130
|||||
Sbjct: 134140 agggggtttcttcttctgactcagaaggcgaccctaacaaggaagagatgaatcg 134193

Score = 48.1 bits (24), Expect = 0.041
Identities = 24/24 (100%)
Strand = Plus / Plus

Query: 1460 aacctcgatccatggcagagccag 1483
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Sbjct: 150396 aacctcgatccatggcagagccag 150419

>AL512429.14.1.11170
Length = 11170

Score = 1159 bits (584), Expect = 0.0
Identities = 588/592 (99%)
Strand = Plus / Plus

Query: 1974 tgattccactcagttacaacagcttcataaccaagtcttactggaacaacaccaattgca 2033
|||||
Sbjct: 4075 tgattccactcagttacaacagcttcataaccaagtcttactggaacaacaccaattgca 4134

Query: 2034 aaaccacctccttcattctcctaaggagtttcctttcarcatgactgttttgaactccaa 2093
|||||
Sbjct: 4135 aaaccacctccttcattctcctaaggagtttcctttcagcatgactgttttgaactccaa 4194

Query: 2094 tgctccccccagcggtgacaacatccartaagcaggtgaagggtccttcatcacagacgtt 2153
|||||
Sbjct: 4195 tgctccccccagcggtgacaacatccagtaagcaggtgaagggtccttcatcacagacgtt 4254

Query: 2154 cagcttggccccggccgaagtattttcttccctccacgaacaccaccgcagcaactgtggc 2213
|||||
Sbjct: 4255 cagcttggccccggccgaagtattttcttccctccacgaacaccaccgcagcaactgtggc 4314

Query: 2214 cccttccagctctccggtgttcactttgagcagcactcctcaaactattcagaggacagt 2273
|||||
Sbjct: 4315 cccttccagctctccggtgttcactttgagcagcactcctcaaactattcagaggacagt 4374

Query: 2274 gagcaaagaaagcctcttagtggtctcaccctctgtgcaaaccaaatctccaggagggt 2333
|||||
Sbjct: 4375 gagcaaagaaagcctcttagtggtctcaccctctgtgcaaaccaaatctccaggagggt 4434

Query: 2334 ttccatccaaaatgagccactcccaccaggcccaacagaacccracaccaccaccattcac 2393
|||||
Sbjct: 4435 ttccatccaaaatgagccactcccaccaggcccaacagaacccracaccaccaccattcac 4494

Query: 2394 attttccatccccagcggaaccagtttcagccccgctgtgtgtccccaattcctgtctc 2453
|||||
Sbjct: 4495 attttccatccccagcggaaccagtttcagccccgctgtgtgtccccaattcctgtctc 4554

Query: 2454 tcctaccagccggattcagaaccagtggtttcctcagctctgttctgccttctctccc 2513
|||||
Sbjct: 4555 tcctaccagccggattcagaaccagtggtttcctcagctctgttctgccttctctccc 4614

Query: 2514 tgccatcccacccacaaatgccatgggrgctgcctagaagtgcaccatccatg 2565
|||||
Sbjct: 4615 tgccatcccacccacaaatgccatggggctgcctagaagtgcaccatccatg 4666

Score = 278 bits (140), Expect = 2e-71
Identities = 140/140 (100%)
Strand = Plus / Plus

Query: 2565 gccatcccagggattagcgaagaaaaatacaaagtctcctcaaccagtgaatgatgataa 2624
|||||
Sbjct: 5332 gccatcccagggattagcgaagaaaaatacaaagtctcctcaaccagtgaatgatgataa 5391

Query: 2625 cattcgtgaaactaagaacgcagtgattcgagacttggggaaaaaaataacttttcagtga 2684
|||||
Sbjct: 5392 cattcgtgaaactaagaacgcagtgattcgagacttggggaaaaaaataacttttcagtga 5451

Query: 2685 tgtcagaccaaaccagcagg 2704
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Sbjct: 5452 tgtcagaccaaaccagcagg 5471

>AC016395.5.1.166869
Length = 166869

Score = 442 bits (223), Expect = e-121
Identities = 226/227 (99%)
Strand = Plus / Minus

Query: 2701 caggagtacaaaatttcaagctttgagcagaggctgatgaatgaaatagagtttcgcttg 2760
|||||
Sbjct: 157129 caggagtacaaaatttcaagctttgagcagaggctgatgaatgaaatagagtttcgcttg 157070

Query: 2761 gaacgtactcctggtgatgaatcagatgatgaaattcaacatgatgagatccccacgggc 2820
|||||
Sbjct: 157069 gaacgtactcctggtgatgaatcagatgatgaaattcaacatgatgagatccccacgggc 157010

Query: 2821 aagtgtattgctcccatctttgacaagagactcaagcacttccgggtcacagaaggctct 2880
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Query: 2881 ccagtcacattcacctgcaaaattggtgggatacctgttccaaaggt 2927
|||||
Sbjct: 156949 ccagttacattcacctgcaaaattggtgggatacctgttccaaaggt 156903

Score = 417 bits (210), Expect = e-113
Identities = 210/210 (100%)
Strand = Plus / Minus

Query: 3284 aggtgagtgggtttaccgcccccgagctgacatggctactcaatggccaacctgtgctac 3343
|||||
Sbjct: 146665 aggtgagtgggtttaccgcccccgagctgacatggctactcaatggccaacctgtgctac 146606

Query: 3344 cagatgcctcccacaagatgctgggtcagggagaccggagtccactctctgctcattgacc 3403
|||||
Sbjct: 146605 cagatgcctcccacaagatgctgggtcagggagaccggagtccactctctgctcattgacc 146546

Query: 3404 cactcactcagcgcgacgcagggacctataagtgcacgctaccaacaaaaccgggcaga 3463
|||||
Sbjct: 146545 cactcactcagcgcgacgcagggacctataagtgcacgctaccaacaaaaccgggcaga 146486

Query: 3464 attcttttagtctggagctctctgtagtag 3493
|||||
Sbjct: 146485 attcttttagtctggagctctctgtagtag 146456

Score = 339 bits (171), Expect = 6e-90
Identities = 171/171 (100%)
Strand = Plus / Minus

Query: 3793 gctcagtggcaccatcagatcccaccgcccattgtctgtccggcccagtggcagtcgctac 3852
|||||
Sbjct: 135746 gctcagtggcaccatcagatcccaccgcccattgtctgtccggcccagtggcagtcgctac 135687

Query: 3853 ggatctctcaccagtaaaggacttgacatattttctgccttttctccatggaaagcacg 3912
|||||
Sbjct: 135686 ggatctctcaccagtaaaggacttgacatattttctgccttttctccatggaaagcacg 135627

Query: 3913 atggtgtattcatgctcttctcggagtgtagtggagagtgatgaacttta 3963
|||||
Sbjct: 135626 atggtgtattcatgctcttctcggagtgtagtggagagtgatgaacttta 135576

Score = 333 bits (168), Expect = 4e-88
Identities = 168/168 (100%)
Strand = Plus / Minus

Query: 3492 agccaaagaggtgaagaaagcacctgtgatcctggagaaactacagaactgcggtgttcc 3551
|||||
Sbjct: 144204 agccaaagaggtgaagaaagcacctgtgatcctggagaaactacagaactgcggtgttcc 144145

Query: 3552 cgaaggccaccccgtagactggagtgccgcgtgataggcatgccccacctgtgttcta 3611
|||||
Sbjct: 144144 cgaaggccaccccgtagactggagtgccgcgtgataggcatgccccacctgtgttcta 144085

Query: 3612 ctggaagaaagacaatgagaccatcccttgaccagagagaggatcag 3659
|||||
Sbjct: 144084 ctggaagaaagacaatgagaccatcccttgaccagagagaggatcag 144037

Score = 306 bits (154), Expect = 9e-80
Identities = 158/159 (99%), Gaps = 1/159 (0%)
Strand = Plus / Minus

Query: 2924 aggtttactggttcaaagatgggaagcagatttctaagagaaatgagcactgcaaaatga 2983
|||||
Sbjct: 151670 aggtttactggttcaaagatgggaagcagatttctaagagaaatgagcactgcaaaatga 151611

Query: 2984 ggcgagaaggagatgggacatgctctctgcacattgaatccactaccagtgatgacgatg 3043
|||||
Sbjct: 151610 ggcgagaaggagatgggacatgctctctgcacattgaatccactaccagtgatgacgatg 151551

Query: 3044 gcaactacaccatcatggcagccaacccccagg-ggaga 3081
|||||
Sbjct: 151550 gcaactacaccatcatggcagccaacccccagggtggaga 151512

Score = 272 bits (137), Expect = 1e-69
Identities = 137/137 (100%)
Strand = Plus / Minus

Query: 3657 cagtatgcaccaggacacaacaggggtatgcctgccttctcattcagccagccaagaaatc 3716
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Sbjct: 139264 cagtatgcaccaggacacaacaggggtatgcctgccttctcattcagccagccaagaaatc 139205

Query: 3717 agacgctggatggtacacgttgtcagccaagaatgaagccggcatcgtgtcgtgcactgc 3776
|||||
Sbjct: 139204 agacgctggatggtacacgttgtcagccaagaatgaagccggcatcgtgtcgtgcactgc 139145

Query: 3777 caggctggatatatacg 3793
|||||
Sbjct: 139144 caggctggatatatacg 139128

Score = 260 bits (131), Expect = 5e-66
Identities = 131/131 (100%)
Strand = Plus / Minus

Query: 3157 aggggaagatcccgagtgcaagaaagagacaaagagcccctacaggaacgctttttccga 3216
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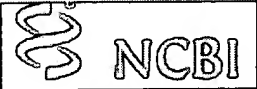
Query: 3217 ccacatttcctgcaggctcctggggatatggtagctcatgaggggcgctctgtcggctg 3276
|||||
Sbjct: 148621 ccacatttcctgcaggctcctggggatatggtagctcatgaggggcgctctgtcggctg 148562

Query: 3277 gactgtaaggt 3287
|||||
Sbjct: 148561 gactgtaaggt 148551

Score = 173 bits (87), Expect = 1e-39
Identities = 87/87 (100%)
Strand = Plus / Minus

Query: 3073 caggggagaaatcagctgttctggccacttgatggtacaaagtttgccattcgagtcgg 3132
|||||
Sbjct: 150584 caggggagaaatcagctgttctggccacttgatggtacaaagtttgccattcgagtcgg 150525

Query: 3133 ctaacctctgctgggtcagtcacagg 3159
|||||
Sbjct: 150524 ctaacctctgctgggtcagtcacagg 150498



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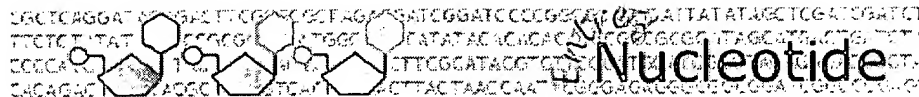
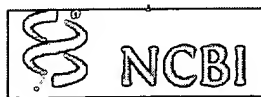
[Links](#)

LOCUS AC024258 160658 bp DNA linear PRI 14-MAY-2002
 DEFINITION Homo sapiens chromosome 10 clone RP11-297N15, complete sequence.
 ACCESSION AC024258
 VERSION AC024258.9 GI:20564414
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 160658)
 AUTHORS Smith,D.R.
 TITLE Genome Therapeutics Corporation Sequencing Center: Human Genome
 Sequence Data
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 160658)
 AUTHORS Smith,D.R.
 TITLE Direct Submission
 JOURNAL Submitted (28-FEB-2000) Genome Therapeutics Corporation, 100 Beaver
 Street, Waltham, MA 02453, USA
 REFERENCE 3 (bases 1 to 160658)
 AUTHORS Smith,D.R.
 TITLE Direct Submission
 JOURNAL Submitted (13-NOV-2001) Genome Therapeutics Corporation, 100 Beaver
 Street, Waltham, MA 02453, USA
 REFERENCE 4 (bases 1 to 160658)
 AUTHORS Smith,D.R.
 TITLE Direct Submission
 JOURNAL Submitted (14-MAY-2002) Genome Therapeutics Corporation, 100 Beaver
 Street, Waltham, MA 02453, USA
 COMMENT On May 14, 2002 this sequence version replaced gi:16905139.
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 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
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 BASE COUNT 50744 a 31675 c 30448 g 47791 t
 ORIGIN

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121 tccttgttcc tacagcagca gaatggatgt tgtattagca ggcataaaaa cattaatctc
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241 tttgaaagca atctttttac tgagcgggtg gtctcaacag tgggcttaag cccatattaa
301 tatattcagt acaccatgct gtaaacagat gagctgtcat ccaggctttg ttgttcatt
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```



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Links

LOCUS AL512429 11170 bp DNA linear PRI 26-OCT-2001

DEFINITION Human DNA sequence from clone RP11-429C3 on chromosome 10, complete sequence.

ACCESSION AL512429

VERSION AL512429.14 GI:16508239

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 11170)

AUTHORS Mashreghi-Mohammadi, M.

TITLE Direct Submission

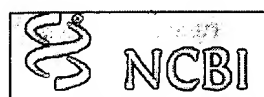
JOURNAL Submitted (26-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

COMMENT On Oct 29, 2001 this sequence version replaced gi:15028699. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr10> RP11-429C3 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pBACe3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-429C3 It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true left end of clone RP11-153K11 is at 9171 in this sequence.



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 TTCTCTATATCTTCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
 TCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
 CACAGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT

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Protein

Genome

Structure

PMC

Taxonomy

OMIM

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Details

Display

Show:

Send to

Get Subsequence

Fe

☐ 1: AC016395. Homo sapiens chro...[gi:20564406]

Links

LOCUS AC016395 166869 bp DNA linear PRI 14-MAY-2002
 DEFINITION Homo sapiens chromosome 10 clone RP11-153K11, complete sequence.
 ACCESSION AC016395
 VERSION AC016395.5 GI:20564406
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 166869)
 AUTHORS Smith,D.R.
 TITLE Genome Therapeutics Corporation Sequencing Center: Human Genome
 Sequence Data
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 166869)
 AUTHORS Smith,D.R.
 TITLE Direct Submission
 JOURNAL Submitted (26-NOV-1999) Genome Therapeutics Corporation, 100 Beaver
 Street, Waltham, MA 02453, USA
 REFERENCE 3 (bases 1 to 166869)
 AUTHORS Smith,D.R.
 TITLE Direct Submission
 JOURNAL Submitted (26-AUG-2000) Genome Therapeutics Corporation, 100 Beaver
 Street, Waltham, MA 02453, USA
 REFERENCE 4 (bases 1 to 166869)
 AUTHORS Smith,D.R.
 TITLE Direct Submission
 JOURNAL Submitted (14-MAY-2002) Genome Therapeutics Corporation, 100 Beaver
 Street, Waltham, MA 02453, USA
 COMMENT On May 14, 2002 this sequence version replaced gi:9929646.
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 /clone_lib="RPCI-11"
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 Frame = +2

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SEP 02 2003

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